

OIKE

RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/879,792

TIME: 10:53:43

Input Set : A:\02973.00035 sequence listing.txt

Output Set: N:\CRF3\06282001\I879792.raw

4 <110> APPLICANT: Xiao, Yonghong
 5 Gedrich, Richard
 7 <120> TITLE OF INVENTION: Regulation of Human Transmembrane Serine
 8 Protease
 10 <130> FILE REFERENCE: 02973.00035
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/879,792
 C--> 12 <141> CURRENT FILING DATE: 2001-06-13
 12 <150> PRIOR APPLICATION NUMBER: US 60/211,224
 13 <151> PRIOR FILING DATE: 2000-06-13
 15 <150> PRIOR APPLICATION NUMBER: US 60/283,353
 16 <151> PRIOR FILING DATE: 2001-04-13
 18 <150> PRIOR APPLICATION NUMBER: US 60/283,648
 19 <151> PRIOR FILING DATE: 2001-04-16
 21 <150> PRIOR APPLICATION NUMBER: PCT _____ (Docket No. LIO-81-WO)
 22 <151> PRIOR FILING DATE: 2001-06-12
 24 <160> NUMBER OF SEQ ID NOS: 36
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 402
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 33 <220> FEATURE:
 34 <221> NAME/KEY: misc_feature
 35 <222> LOCATION: (1)...(402)
 36 <223> OTHER INFORMATION: n = A,T,C or G
 38 <400> SEQUENCE: 1
 39 aatgcccttc ccagcgggtat atctccctcc agtgttccca ctgcggactg agggccatga 60
 40 ccggggcggat cgtgggaggg gcgctggcct cggatagcaa gtggccttgg caagtgaagcc 120
 41 tgcacttcgg caccaccac atctgtggag gcacgtcat tgacgccag tgggtgtca 180
 W--> 42 ctncgcacca ctgttcttc gtgnaccgg gagaaggtcc tggagggctg gaaggtgtac 240
 43 gcgggcacca gcaacctgca ccagttgcct gaggcagcct ccattgccga gatcatcatc 300
 44 aacagcaatt acaccgatga ggaggacgac tatgacatcg ccctcatgcy gctgttcaag 360
 W--> 45 ncccttgacc ctgttcgggt gaggaattt tgcatttccc gt 402
 47 <210> SEQ ID NO: 2
 48 <211> LENGTH: 285
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 2
 53 ccatgaccgg gcggtatcgtg ggagggggcgc tggcctcgga tagcaagtgg ccttggcaag 60
 54 tgagtctgca ctctggcacc acccacatct gtggaggcac gtcattgac gccagtgagg 120
 55 tgetcactgc cgccactgc ttcttcgtga cccgggagaa ggtcctggag ggctggaagg 180
 56 tgtacgggg caccagcaac ctgcaccagt tgcttgaggc agcctccatt gccgagatca 240
 57 tcatcaacag caattacacc gatgaggagg acgactatga catcg 285
 59 <210> SEQ ID NO: 3
 60 <211> LENGTH: 600
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Homo sapiens

ENTERED

See p.5

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64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <222> LOCATION: (1)...(600) /
67 <223> OTHER INFORMATION: n = A,T,C or G
69 <400> SEQUENCE: 3
70 gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggcagcctcc      60
71 attgccgaga tcatcatcaa cagcaattac accgatgagg aggacgacta tgacatcgcc      120
72 ctcatgcggc tgtccaagcc cctgaccctg tccggtgagg gaatctgcac tccccgtct      180
73 cctgcccccc agccccagca ccctctgcag ccctcgcaact tgtcagcatc tgtcaactca      240
74 tatccggggc ccaaagcttc tgcagggcag aagtcaaaga ctcttaaaga tccttacatg      300
75 gaacacttct gttttataat tagggaaact gaagcccaag ggttataaat aagtttgctc      360
76 caaatgacac atctcacatt acaaattgat gacggagtca gggcttgggt actgatctta      420
77 atcaatagat tgaattcttt cactggtatt aactgagcac ctagggggcca aacgctatgg      480
78 taggcatttc acacatatga ttctatttac tcttcacaac caaccctgtg gagcaggcac      540
W--> 79 tattattaac ttcatttgac atatgangaa atggagcttt acagagagat aattacctga      600
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 591
83 <212> TYPE: DNA
84 <213> ORGANISM: Homo sapiens
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (1)...(591) /
89 <223> OTHER INFORMATION: n = A,T,C or G
91 <400> SEQUENCE: 4
92 gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggcagcctcc      60
93 attgccgaga tcatcatcaa cagcaattac accgatgagg aggacgacta tgacatcgcc      120
94 ctcatgcggc tgtccaagcc cctgaccctg tccggtgagg gaatctgcac tccccgtct      180
95 cctgcccccc agccccagca ccctctgcag ccctcgcaact tgtcagcatc tgtcaactca      240
96 tatccggggc ccaaagcttc tgcagggcag aagtcaaaga ctcttaaaga tccttacatg      300
97 gaacacttct gttttataat tagggaaact gaagcccaag ggttataaat aagtttgctc      360
98 caaatgacac atctcacatt acaaattgat gacggagtca gggcttgggt actgatctta      420
99 atcaatagat tgaattcttt cactggtatt aactgagcac ctagggggcca aacgctatgg      480
W--> 100 taggcatttc acacatatga ttctatttac tcttcacaac caaccctgtg gagcangcac      540
W--> 101 tattattaac ttcatttgac atatgangaa atggagcttt acagagagat a      591
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 286
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 5
109 gcgatgtcat agtcgtcctc ctcatcggcg taattgctgt tgatgatgat ctcggaatg      60
110 gaggtgcct caggcaactg gtgcaggttg ctggtgcccg cgtacacctt ccagccctcc      120
111 aagaccttct cccgggtcac gaagaagcag tgggcggcag tgagcaccga ctgggcgtca      180
112 atgagcgtgc ctccacagat gtgggtggtg ccgaagtgtc gactcacttg ccaaggccac      240
113 ttgctattcg aggccagcgc cccttccacg attcgcccgg tcatgg      286
115 <210> SEQ ID NO: 6
116 <211> LENGTH: 384
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 6

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121 gagggctgga aggtgtacgc gggcaccagc aacctgcacc agttgcctga ggagcctcca      60
122 ttgccgagat catcatcaac agcaattaca ccgatgagga ggacgactat gacatgcccc      120
123 tcatgcggct gtccaagccc ctgacctgt ccggtgaggg aatctgcaact cccgctctc      180
124 ctgcccccca gccccagcac cctctgcagc cctgcactt gtcagcatct gtoaactcat      240
125 atccggggcc caaagcttct gcagggcaga agtcaaagac tcttaaagat cttacatgg      300
126 aacacttctg ttttataatt agggaaactg aagcccaagg gttataaata agtttgctcc      360
127 aaatgacaca tctcacatta caaa                                         384
129 <210> SEQ ID NO: 7
130 <211> LENGTH: 471
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
135 <221> NAME/KEY: misc_feature
136 <222> LOCATION: (1)...(471) /
137 <223> OTHER INFORMATION: n = A,T,C or G
139 <400> SEQUENCE: 7
W--> 140 tttttttttt nttttttttt ttggagcaaa cttatttana acccttgggc ttcagttnc      60
W--> 141 ctaattataa aacagaagtn tnccatgtaa ggncttnaa gagtctttga cttctgccct      120
142 gcagaagctt tggggcccg atatgagttg acagatgctg acaagtgcga gggctgcaga      180
W--> 143 gggtnctggg gctggggggc aggagagcgg ggagtgcaga ttcctcacc ggacagggtc      240
W--> 144 aggggnttgg acagccgcat gagggcgatg tcatagtcgt cctcctcatc ggtgtaatnn      300
W--> 145 ctnttgatga tgatctcggc aatggaggct gcctcaggca actgggtnc      360
W--> 146 tnccncgta acaccttcca gccntccagg nccttttccc gggtcacgaa gaagcagtng      420
W--> 147 ggccgcaatt agcaccact ggggggtcaat gaggtgccn ccacanattt g      471
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 235
151 <212> TYPE: DNA
152 <213> ORGANISM: Homo sapiens
154 <400> SEQUENCE: 8
155 gggctggaag gtgtacgcgg gcaccagcaa cctgcaccag ttgcctgagc agcctccatt      60
156 gccgagatca tcatcaacag caattacacc gatgaggagg acgactatga catcgccctc      120
157 atgcggctgt ccaagccctt gacctgtcc ggtgagggaa tctgcactcc ccgctctcct      180
158 gccccccagc cccagcacc tctgcagccc tcgcacttgt cagcatctgt caact      235
160 <210> SEQ ID NO: 9
161 <211> LENGTH: 19
162 <212> TYPE: DNA
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 9
166 ctgccagcag ctgggtttc                                         19
168 <210> SEQ ID NO: 10
169 <211> LENGTH: 20
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
173 <400> SEQUENCE: 10
174 aggtttcct ggatggtgga                                         20
176 <210> SEQ ID NO: 11
177 <211> LENGTH: 1748
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens

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181 <400> SEQUENCE: 11
182 ctcagagacc atggagaggg acagccacgg gaatgcatct ccagcaagaa caccttcagc      60
183 tggagcatct ccagcccagg catctccagc tgggacacct ccaggccggg catctccagc      120
184 ccaggcatct ccagcccagg catctccagc tgggacacct ccgggcccgg catctccagc      180
185 ccaggcatct ccagctggta cactccagg ccgggcatct ccaggccggg catctccagc      240
186 ccaggcatct ccagcccagg catctccagg tctggcatca ctttccagg cctcatccgg      300
187 caggtcata tccgcccagg cagcctcggg gacaacctcc ccaaccagag tgtaccttgt      360
188 tagagcaaca ccagtggggg ctgtacccat ccgatcatct cctgccagg cagcaccagc      420
189 aaccaggggc accaggggaga gccagggtac gagcctgccc aagttcacct ggcgggagg      480
190 ccagaagcag ctaccgctca tgggtgctg gctcctcctc attgccctgg tggtttcgct      540
191 catcactctc ttccagttct ggcaggggcca cacagggatc aggtacaagg agcagaggga      600
192 gagctgtccc aagcacgctg ttctgctgtg cggggtgggt gactgcaagc tgaagagtga      660
193 cgagctgggc tgcgtgaggt ttgactggga caagtctctg cttaaaatct actctgggtc      720
194 ctcccatcag tggcttccca ctgttagcag caactggaat gactcctact cagagaagac      780
195 ctgccagcag ctgggtttcg agagtgtcga ccggacaacc gaggttgccc acagggattt      840
196 tgccaacagc ttctcaatct tgagatacaa ctccaccatc caggaaagcc tccacaggtc      900
197 tgaatgcctt tccagcgggt atatctccct ccagtgttcc cactgcggac tgagggccat      960
198 gaccggggcg atcgtgggag gggcgttggc ctcgatagc aagtggcctt ggcaagtga      1020
199 tctgcacttc ggcaccaccc acatctgttg aggcacgctc attgacgcc agtgggtgct      1080
200 cactgccgcc cactgcttct tctgacccg ggagaaggte ctggagggtt ggaagggtga      1140
201 cgcgggcacc agcaacctgc accagttgcc tgaggcagcc tccattgcc agatcatcat      1200
202 caacagcaat tacaccgatg aggaggacga ctatgacatc gccctcatgc ggctgtccaa      1260
203 gccctgacc ctgtccgctc acatccaccc tgcctgcctc cccatgcag gacagacctt      1320
204 tagcctcaat gagacctgct ggatcacagg ctttggcaag accagggaga cagatgacaa      1380
205 gacatccccc ttctccggg aggtgcaggt caatctcatc gacttcaaga aatgcaatga      1440
206 ctacttggtc tatgacagtt accttaccct aaggatgatg tgtgctggg accttcgtgg      1500
207 gggcagagac tctgccagg gagacagcgg ggggcctctt gtctgtgagc agaacaaccg      1560
208 ctggtacctg gcagggtgtc ccagctgggg cacaggctgt ggccagagaa acaaacctgg      1620
209 tgtgtacacc aaagtgcag aagttcttcc ctggatttac agcaagatgg agagcgaggt      1680
210 gcgattcaga aaatcctaac cagc' act gctgctctgc acagcaccgg ctgctgtgac      1740
211 tcgagaaa
213 <210> SEQ ID NO: 12
214 <211> LENGTH: 562
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 12
219 Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser
220 1 5 10 15
221 Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly
222 20 25 30
223 Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly
224 35 40 45
225 Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr
226 50 55 60
227 Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
228 65 70 75 80
229 Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
230 85 90 95
231 Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr

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232          100          105          110
233 Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
234          115          120          125
235 Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
236          130          135          140
237 Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
238 145          150          155          160
239 Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
240          165          170          175
241 Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr
242          180          185          190
243 Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
244          195          200          205
245 Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe
246          210          215          220
247 Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln
248 225          230          235          240
249 Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys
250          245          250          255
251 Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val
252          260          265          270
253 Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser
254          275          280          285
255 Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr
256          290          295          300
257 Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg
258 305          310          315          320
259 Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val
260          325          330          335
261 Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp
262          340          345          350
263 Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu
264          355          360          365
265 Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His
266          370          375          380
267 Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn
268 385          390          395          400
269 Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser
270          405          410          415
271 Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met
272          420          425          430
273 His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
274          435          440          445
275 Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
276          450          455          460
277 Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
278 465          470          475          480
279 Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
280          485          490          495

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35